46

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999 TIME: 14:06:48

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1 2		SEQUENCE LISTING	ENTERED
3	(1) G	eneral Information:	
5 6 7 8	(i)	APPLICANT: Malcolm, Bruce Taremi, Shahriar S. Weber, Patricia Yao, Nanhua	
10 11 12	(ii)	TITLE OF INVENTION: Covalent Complexes of Hepat NS3 Protease and NS4A Cofactor Peptide	titis C Virus
13 14	(iii)	NUMBER OF SEQUENCES: 123	
15 16 17 18 19 20 21	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Schering-Plough Corp. (B) STREET: 2000 Galloping Hill Road (C) CITY: Kenilworth (D) STATE: New Jersey (E) COUNTRY: USA (F) ZIP: 07030	
22 23 24 25 26 27 28	. ` `	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: Power Macintosh (C) OPERATING SYSTEM: 8.0.1 (D) SOFTWARE: Microsoft Word 6.0.1	
29 30 31 32 33		CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 09/198,723 (B) FILING DATE: 24 NOV 1998 (C) CLASSIFICATION:	
34 35 36 37 38	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: McLaughlin, Jaye P. (B) REGISTRATION NUMBER: 41,211 (C) REFERENCE/DOCKET NUMBER: JB0800	
39 40 41 42 43 44 45	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (908)298-5056 (B) TELEFAX: (908)298-5388	

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47 48	(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:1	:							
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61 62	Arg	GIY	ser	His 20	мес	GIA	Ser	vат	25	тте	val	сту	Arg	30	тте	Leu
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64	Ser	Glv	Ser	Gly	Sar	Tla	Thr	λΙລ	ጥህጉ	Sar	Gl n	@l n	Thr	Ara	G] v	T.011
65	Der	GLY	35	GLY	Ser	116	1111	40	171	Der	QIII	GIII	45	Arg	OLY	БСС
66			33										10			
67	Leu	Glv	Cvs	Ile	Ile	Thr	Ser	Leu	Thr	Glv	Ara	Asp	Lvs	Asn	Gln	Val
68		50	- 2				55				3	60	-1-			
69					•											
70	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala
71	65	_				70					75					80
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73	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser
74					85					90					95	
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76	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly		Ile	Thr	Gln	Met	_	Thr	Asn
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80	Val	ASP	115	ASP	rea	Val	сту	120	GIII	Ата	PIO	PIO	125	Ald	Arg	Ser
81			113					120					125			
82	Leu	Thr	Pro	Cys	Thr	Cvs	Glv	Ser	Ser	Asp	Leu	Tvr	Leu	Val	Thr	Ara
83		130		-1-		-1-	135			F		140				5
84																
85	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser
86	145		_			150		_		_	155	_		_	_	160
87																
88	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly
89					165					170					175	
90																
91	Pro	Leu	Leu		Pro	Ser	Gly	His		Val	Gly	Ile	Phe	_	Ala	Ala
92				180					185					190		
93		_	1	_				_			_	_,		_		
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124		50					55					60				
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126		Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala
127	65					70					75					80
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129	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser
130					85					90					95	
131																
132	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn
133				100					105					110		
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135	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser
136			115	_			_	120					125		_	
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138	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg
139		130		•		-	135			-		140				
140																
141	His	Ala	Asp	Val	Ile	Pro	Val	Ara	Ara	Ara	Glv	Asp	Ser	Ara	Glv	Ser
142	145		E			150		9	9	5	155			9	1	160
143																
144	T.em	Leu	Ser	Pro	Δra	Pro	Val	Ser	Tur	T.e.11	T.vs	Glv	Ser	Ser	Glv	Gly
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153	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser								
154		210					215									
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170	Met	Glv	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Glv	ī.eu	Val	Pro
171	1	0_1		-	5					10	501	501	01,	200	15	
172	_				_											
173	Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
174	_	_		20		_			25			-	_	30		
175																
176	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu
177			35					40					45			
178		_		_											_	_
179	Leu	_	Cys	Ile	Lys	Thr		Leu	Thr	Gly	Arg	_	Lys	Asn	Gln	Val
180		50					55					60				
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184	0.5					70					75					80
185	Thr	Cvs	Val	Asn	Glv	Val	Cvs	Trp	Thr	Val	Tur	His	Glv	Δla	ดโซ	Ser
186		-,-			85		0,2			90	- 1 -		- 1		95	
187																
188	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn
189				100	_		_	_	105					110		
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191	Val	Asp		Asp	Leu	Val	Gly		Gln	Ala	Pro	Pro		Ala	Arg	Ser
192			115					120					125			
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194	Leu		Pro	cys	Thr	cys		Ser	ser	Asp	Leu		Leu	vaı	unr	Arg
195 196		130					135					140				
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198	145	AIG	АЗР	Val	116	150	Val	Arg	Arg	ALG	155	ASP	Ser	Arg	СТУ	160
199	113					130					133					100
200	Leu	Leu	Ser	Pro	Ara	Pro	Val	Ser	Tvr	Leu	Lvs	Glv	Ser	Ser	Glv	Gly
201					165				-] -	170	_,.	1			175	1
202																
203	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala
204				180			=		185		_			190		
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206 207 208	Val	Cys	Thr 195	Arg	Gly	Val	Ala	Lys 200	Ala	Val	Asp	Phe	Val 205			Glu
209	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser								
210		210					215									
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215	(2)	INF	ORMA'	TION	FOR	SEQ	ID I	NO:4	:							
216																
217			(i):			CHAI										
218						NGTH				acid	5					
219						PE: 8										
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224		(:	xi):	SEQUI	ENCE	DES	CRIP	rion	: SE	O ID	NO:	1:				
225				_												
226	_	Gly	Ser	Ser		His	His	His	His		Ser	Ser	Gly	Leu		Pro
227	1				5					10					15	
228			_										_			_
229	Arg	СТĀ	Ser		мет	Gly	Ser	Val		Ile	val	GTÄ	Arg		ITe	Leu
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232	Ser	СТĀ		СТĀ	Ser	Ile	Thr		Tyr	Ser	GIn	GIn		Arg	GTA	Leu
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244	Luc	Thr	T. 211	λla	G] v	Pro	T. 17 C	Gl v	Dro	Tla	Thr	Gl n	Mo+	Фиг	Фhr	λen
245	цуз	1111	пец	100	СТУ	110	пуз	Gry	105	TTC	1111	GIII	Mec	110	1111	ASII
246				100					103					110		
247	va1	Δsn	Gln	Δsn	Leu	Val	Glv	Trn	Gln	Δla	Pro	Pro	G] v	Δla	Δra	Ser
248	• • • •	nop.	115		LCu		013	120	0111	niu	110	110	125	AIU	n. 9	501
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251		130		0,0		0,5	135	201	501	p	200	140	200	***	****	*** 9
252		130					133					140				
253	His	Δla	Δsn	Val	Tle	Pro	Val	Δra	Δτα	Δra	Glv	Δsn	Ser	Δra	Glv	Ser
254	145		_P			150		9	9	9	155	p	201	9	1	160
255	-10															
256	Leu	Leu	Ser	Pro	Ara	Pro	Val	Ser	Tvr	Leu	Lvs	Glv	Ser	Ser	G] v	Glv
257					165			~~~	-] ~	170	-,5	1	~~.	~~1	175	 1
258										•						
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***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

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4116	(2)	INF	ORMA'	I'ION	FOR	SEQ	ID 1	NO: 92	2:								
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4130			(1	B) LO	CAT:	ION:	16	551									
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4133		(xi) SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID NO	0:92	:					
4134																	
4135									CAT								48
4136		Gly	Ser	Ser		His	His	His	His		Ser	Ser	Gly	Leu		Pro	
4137	1				5					10			٠		15		
4138																	
4139									GTT								96
4140	Arg	GTA	Ser		Met	GTĀ	Ser	Va⊥	Val	IIe	Val	GTÀ	Arg		IIe	Leu	
4141				20			•		25					30			
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4143									TAC								144
4144 4145	ser	сту	35	GIY	Ser	TTe	THE	40	Tyr	Ser	GIN	GIN	45	Arg	GIY	ьeu	
4145			33					40					43				
4147	СФФ	сст	ሞሮሮ	ልጥሮ	ልጥሮ	λCͲ	AGC	տրդո Մ	ACA	aac	caa	GAC	AAG	ልልሮ	CAG	GTC.	192
4148									Thr								172
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4150		•															
4151	GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
4152									Thr								
4153	65					70					75					80	
4154																	
4155	ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
4156	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
4157		-			85		-	-		90	-		-		95		
4158																	
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4160	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
4161	-			100	-		-	_	105					110			
4162																	

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4163	GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	ccc	CCC	GGG				384	
4164												Pro						
4165			115				1	120					125		5			
4166																		
4167	ጥጥር	ACA	CCA	TGC	ACC	ጥርጥ	GGC	AGC	тса	GAC	Стт	TAC	ጥጥር	GTC	ACG	ΔGA	432	
4168												Tyr					452	
4169	пец	130	110	Cys	1111	Cys	135	Ser	Der	ASP	пеа	140	пеа	Val		Arg		
4170		130					133					140						
4171	CAM	CCD	CAC	OTT C	y mm	caa	CITIC	000	aaa	aaa	aaa	GAC	» am	3.00	aaa	N.C.C	400	
																	480	
4172 4173		АТА	ASP	νат	TTE	150	Vат	ALG	Arg	ALG	_	Asp	Ser	AIG	GIY			
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4175												GGC					528	
4176	Leu	Leu	ser	Pro	_	Pro	vaı	ser	Tyr		rAz	Gly	ser	ser	_	GTA		
4177					165					170					175			
4178						maa												
4179												ATC					576	
4180	Pro	Leu	Leu	_	Pro	Ser	GTA	His		Val	GTÀ	Ile	Phe	_	Ala	Ala		
4181				180					185					190				
4182																		
4183												TTT					624	
4184	Val	Cys		Arg	GTÀ	Val	АТа	-	АТа	Val	Asp	Phe		Pro	Val	GLu		
4185			195					200					205					
4186																		
4187				ACT					TGA								651	
4188	Ser		Glu	Thr	Thr	Met	_	Ser										
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4869	(2)	INF	DRMA'	TION	FOR	SEO	ID 1	NO:10	02:					- \ 			<u></u>	
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4876 4877 4878 4879 4880			(1) MOI) FE	D) TO LECUI ATURI	OPOLO	OGY: VPE:	cDN	ear										
4876 4877 4878 4879 4880 4881			(1) MOI) FE	D) TO LECUI ATURI A) NA	OPOLO LE TY E: AME/I	OGY: VPE: KEY:	cDNA	ear Ì										
4876 4877 4878 4879 4880			(1) MOI) FE	D) TO LECUI ATURI	OPOLO LE TY E: AME/I	OGY: VPE: KEY:	cDNA	ear Ì										
4876 4877 4878 4879 4880 4881 4882 4883			(1) MOI) FE	D) TO LECUI ATURI A) NA	OPOLO LE TY E: AME/I	OGY: VPE: KEY:	cDNA	ear Ì										
4876 4877 4878 4879 4880 4881 4882 4883		(ix	(1) MOI) FEA (1	D) TO LECUI ATURI A) NI B) LO	OPOLO LE TY E: AME/I	OGY: VPE: KEY: ION:	CDS	ear	gle	ID NO	o:102	2:						
4876 4877 4878 4879 4880 4881 4882 4883 4884		(ix	(1) MOI) FEA (1	D) TO LECUI ATURI A) NA	OPOLO LE TY E: AME/I	OGY: VPE: KEY: ION:	CDS	ear	gle	ID NO	D: 102	2:						
4876 4877 4878 4879 4880 4881 4882 4883 4884 4885	ΑΨС	(ix	(1)) MOI) FEA (1) (1)) SE(D) TO LECUI ATURI A) NI B) LO	DPOLO LE TY E: AME/I DCATI	OGY: YPE: KEY: ION:	CDS	ear A	gle SEQ :				GGC	СТС	GTG	CCG	48	
4876 4877 4878 4879 4880 4881 4882 4883 4884 4885 4886		(ix (xi GGC	(1)) MO1) FEA (1) (1)) SEQ AGC	D) TO LECUI ATURI A) NI B) LO QUENO AGC	DPOLO LE TY E: AME/I DCATI CE DE	OGY: VPE: CEY: CON: CAT	CDS 1	ear A L998 ON: S	gle SEQ :	CAC	AGC	AGC					48	
4876 4877 4878 4879 4880 4881 4882 4883 4884 4885 4886 4887	Met	(ix (xi GGC	(1)) MO1) FEA (1) (1)) SEQ AGC	D) TO LECUI ATURI A) NI B) LO QUENO AGC	CE DE CAT His	OGY: VPE: CEY: CON: CAT	CDS 1	ear A L998 ON: S	gle SEQ :	CAC His	AGC				Val		48	
4876 4877 4878 4879 4880 4881 4882 4883 4884 4885 4886 4887 4888		(ix (xi GGC	(1)) MO1) FEA (1) (1)) SEQ AGC	D) TO LECUI ATURI A) NI B) LO QUENO AGC	DPOLO LE TY E: AME/I DCATI CE DE	OGY: VPE: CEY: CON: CAT	CDS 1	ear A L998 ON: S	gle SEQ :	CAC	AGC	AGC					48	
4876 4877 4878 4879 4880 4881 4882 4883 4884 4885 4886 4887	Met 1	(ix (xi GGC Gly	(1)) MOI) FEA (1)) SEC AGC Ser	D) TO LECUI ATURI A) NA B) LO QUENO AGC Ser	E: AME/I CE DI CAT His	CAT His	CDS 1 CPTIC CAT His	L998 ON: : CAT His	SEQ : CAT His	CAC His 10	AGC Ser	AGC	Gly	Leu	Val 15	Pro	48	

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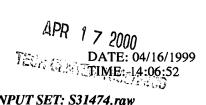
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4892	Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	
4893	_			20					25					30			
4894																	
4895	TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	144
4896	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	
4897			35					40					45				
4898																	
4899	CTT	GGT	TGC	ATC	ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC .	192
4900	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	
4901		50	-				55					60					
4902																	
4903	GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
4904	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Ļeu	Ala	
4905	65	_				70					75					80	
4906																	
4907	ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
4908	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
4909		_			85					90					95		
4910							•										
4911	AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	336
4912	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
4913	_			100					105					110			
4914																	
4915	GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
4916	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
4917		_	115					120					125				
4918																	
4919					ACC												432
4920	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
4921		130					135					140					
4922																	
4923	CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
4924	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly		
4925	145					150					155					160	
4926																	
4927	CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	528
4928	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser		Gly	
4929					165					170					175		
4930																	
4931	CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
4932	Pro	Leu	Leu		Pro	Ser	Gly	His		Val	Gly	Ile	Phe		Ala	Ala	
4933				180					185					190			
4934																~~~	624
4935	GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
4936	Val	Cys	Thr	Arg	Gly	Val	Ala			Val	Asp	Phe			Val	Glu	
4937			195					200					205				
4938																	
4939																TCC	672
4940	Ser	Met	Glu	Thr	Thr	Met			Pro	Val	Phe			Asn	Ser	Ser	
4941		210					215					220					
4942																	500
4943	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
4944	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	۷al	Ala	His	Leu	His	Ala	Pro	

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4945 4946	225					230					235					240	
4947	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
4948	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
4949		_		_	245			-		250			-		255		
4950																	
4951	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
4952	Glv	Tvr	Lvs	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
4953	2	- 2 -		260					265					270		-	
4954																	
4955	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
4956	Phe	Gly	Ala	Tvr	Met	Ser	Lvs	Ala	His	Glv	Ile	Asp	Pro	Asn	Ile	Arq	
4957		-	275	-			-	280		-		-	285			-	
4958																	
4959	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
4960	Thr	Gly	Val	Arq	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
4961		290					295		•			300		•			
4962																	
4963	TÁT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
4964	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
4965	305	_	_			310	_	_	_	_	315	_				320	
4966																	
4967	ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
4968	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
4969					325					330					335		
4970																	
4971	GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
4972	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
4973				340					345					350			
4974																	
4975						GCT											1104
4976	Val	Val		Ala	Thr	Ala	Thr		Pro	Gly	Ser	Val		Val	Pro	His	
4977			355					360					365				
4978																	
4979						GTG											1152
4980	Pro		Ile	GLu	GLu	Val		Leu	Ser	Asn	Thr	_	GLu	Ile	Pro	Phe	
4981		370					375					380					
4982								~	~~~			~~~	~~>		a.m	ama	1000
4983						CCC											1200
4984						Pro											
4985	303					390					395					400	
4986 4987	a mm	mma	mam	a a m	шаа				шаа	~~~	a.a		000	aas	220	аша	1040
4988						AAG											1248
4988	тте	rne	CAR	UTS		Lys	гуз	гÀг	Cys	_	GIU	ьeu	WTG	ATG	LуS 415	rea	
4909					405					410					413		
4991	ም ር እ	aaa	משמ	GG N	איייר	AAC	CCT	CTC	aaa	mиm	ጥአጣ	מממ	aaa	CTC	Gλm	GT/G	1296
4991						Asn											1.2 30
4993	251	GTÄ	пeп	420	TTG	HOII	ATO	val	425	TÄT	TAT	Arg	GTÀ	430	rah	VOL	
4994				740					743					±20			
4995	ሞሮሮ	CTC	מידע	CCA	ልሮሞ	ATC	GGA	GAC	GT/C	Стт	CTC	QTO.	GC A	ΔCA	GAC	GCT	1344
4996						Ile											1344
4997	~~_		435				1	440					445		_P		

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4998																	
4999	СТС	ΔTG	ACG	GGC	ጥልጥ	ACG	GGC	GAC	ттт	GAC	тсδ	GTG	ΔТС	GAC	тст	AAC	1392
5000									Phe								10,1
5001	пса	450		OL y	- 7 -	****	455	иор	1110	тор	JCI	460	110	пор	0,5		
5002		100					133					400					
5002	A C A	mam.	CTC	N.C.C	CAC	202	CTC.	CAC	TTC	N.C.C	mma	CAM	aaa	אממ	ጥሞር	A C C	1440
5003									Phe								1440
		Cys	Val	1111	GIH		vaı	ASP	File	ser		ASP	PIO	IIII	FIIE	480	
5005	465					470					475					400	
5006	* mm	a.a	3.00	3.00	100	ama	aam	a.,	a.a	aa.	ama	maa	999	maa	a • a	000	1400
5007									GAC								1488
5008	тте	GIU	Thr	Inr		vaı	Pro	GIN	Asp		νа⊥	ser	Arg	ser		arg	
5009					485					490					495		
5010																	
5011									AGA								1536
5012	Arg	GTÀ	Arg		GTÀ	Arg	GTA	Arg	Arg	GTÀ	IIe	Tyr	Arg		Val	Thr	
5013				500					505					510			
5014																	
5015									TTC								1584
5016	Pro	Gly		Arg	Pro	Ser	Gly		Phe	Asp	Ser	Ser		Leu	Cys	Glu	
5017			515					520					525				
5018																	
5019									TAC								1632
5020	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	\mathtt{Trp}	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	
5021		530					535					540					
5022																	
5023	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	1680
5024	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	
5025	545					550					555					560	
5026											•					•	
5027									AGT								1728
5028	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	
5029					565					570					575		
5030															•		
5031	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	1776
5032	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	
5033				580					585					590			
5034																	
5035	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	1824
5036	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	
5037			595					600					605				
5038																	
5039	CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	1872
5040	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	
5041		610					615			_		620					
5042										•							
5043	CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	ĠGA	GCC	GTC	1920
5044	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	
5045	625				-	630					635	_		_		640	
5046																	
5047	CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA	1968
5048									Pro								
5049					645					650		4	4		655		
5050										-							

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998
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6609			115					120					125				
6610																	
6611	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	432
6612	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	
6613		130					135					140					
6614																	
6615						AGA											480
6616	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	•
6617	145					150					155					160	
6618																	
6619						AGC											528
6620	GLY	Asp	Ser	Arg		Ser	Leu	Leu	Ser		Arg	Pro	Val	Ser	_	Leu	
6621					165					170					175		
6622																	
6623						GGT											576
6624	гàг	GTÅ	ser		GTĀ	Gly	Pro	Leu		cys	Pro	ser	СТА		Ата	val	
6625				180					185					190			
6626	000	N MC	mma	000	aam	000	am s	maa	3.00	a aa		amm	~~~		~~~	ama	604
6627						GCC											624
6628 6629	GIY	тте		Arg	АТА	Ala	val		Thr	Arg	GTĀ	vaı		гàг	Ата	vaı	
6630			195					200					205				
6631	GAC	արար	CTC.		CTLY	GAG	TICC	አመሮ	CAA	A CITT	х ст	N TO CO	aaa	mam	aaa	OTT C	672
6632						Glu											672
6633	кор	210	Val	110	Val	GIU	215	Mec	GIU	1111	1111	220	ALG	Ser	FIO	Val	
6634		210					213					220					
6635	ጥጥሮ	ACG	GAC	AAC	ጥ ሮ Δ	TCC	כככ	CCG	פככ	сπа	ככפ	CAG	שרט.	արար	CAA	GTG.	720
6636	_	_				Ser											720
6637	225				201	230			niu	· u ·	235	0111	501	1110	0111	240	
6638						200					233		•			240	
6639	GCC	CAC	СТА	CAC	GCT	CCC	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	768
6640						Pro											
6641					245			1		250	-1-			-1-	255		
6642																	
6643	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	816
6644						Gln											
6645			_	260			_	_	265					270			
6646																	
6647	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	864
6648	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	
6649			275					280					285				
6650																	
6651						AGA											912
6652	Ile		Pro	Asn	Ile	Arg		Gly	Val	Arg	Thr		Thr	Thr	Gly	Ala	
6653		290					295					300					
6654																	
6655						ACC											960
6656		Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe		Ala	Asp	Gly	Gly	_	
6657	305					310					315					320	
6658	m					<u>.</u>											
6659	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	A'l'A	TGT	GAT	GAG	TGC	CAT	TCA	ACT	1008

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6660 6661	Ser	Gly	Gly	Ala	Tyr 325	Asp	Ile	Ile	Ile	Cys 330	Asp	Glu	Cys	His	Ser 335	Thr	
6662 6663 6664	GAC Asp	TCG Ser	ACT Thr	ACA Thr	ATC Ile	TTG Leu	GGC Gly	ATC Ile	GGC Gly	ACA Thr	GTC Val	CTG Leu	GAC Asp	CAA Gln	GCG Ala	GAG Glu	1056
6665 6666	_			340					345					350			1104
6667 6668	ACG Thr	GCT Ala	Gly	GCG Ala	CGG Arg	CTT Leu	GTC Val	GTG Val 360	CTC	GCC Ala	ACC	Ala	Thr 365	Pro	Pro	GGA	1104
6669 6670			355	ama	CCA	a s a	aa s		እሞሮ	GAG	GNG	GTG.		CTG	тст	ААТ	1152
6671 6672 6673	Ser	Val	Thr	Val	Pro	His	Pro 375	Asn	Ile	Glu	Glu	Val 380	Ala	Leu	Ser	Asn	
6674																.	1200
6675	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	ATC	CCC	A'I''I'	GAA	Δla	Tle	1200
6676 6677 6678	385				Pro	390					395					400	
6679	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	1248
6680	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys		Ser	Lys	Lys	Lys	Cys 415	Asp	
6681					405					410					113		
6682 6683	GNG	CTC	GCC	GCA	AAG	СТС	TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	1296
6684	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	
6685				420				-	425					430			
6686																	1244
6687	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	1344
6688	Tyr	Arg			Asp	Val	Ser			Pro	Thr	ile	G19 445	Asp	vaı	Val	
6689			435					440					443				
6690	аша	аша	aa s	אמא	CAC	G C T	CTG	ΔТС	۸cg	GGC	ጥልጥ	ACG	GGC	GAC	TTT	GAC	1392
6691 6692	Unl	Ual	ΔCA	Thr	Agn	Δla	Leu	Met	Thr	Glv	Tvr	Thr	Gly	Asp	Phe	Asp	
6693	Val	450		1111	ASP	ALG	455			1	- 1 -	460		_		_	
6694																	
6695	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	1440
6696	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	
6697	465					470					475					480	
6698											3.00	o mo	. aan	י מא	G A C	GC A	1488
6699	TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	Mb w	The	UTU:	Dro	CAR	. Δer	GCA Ala	1400
6700	Leu	Asp	Pro	'l'nr			тте	GIU	THE	490		Val	. FIC		495	1111	
6701					485					4 70					•		
6702 6703	QTQ	י ייירים	י ממר	י ייירים	י כאס	CGG	cgg	GGT	AGG	ACT	' GGC	AGG	GGT	AGO	AGA	GGC	1536
6704	Val	Ser	Aro	Ser	Gln	Arc	Arc	Gly	Arg	Thr	Gly	Arg	Gly	Arg	g Arg	gly	
6705	, , ,		5	500		_	, ,	•	505		_			510)		
6706																	
6707	ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG	CCC	TCC	GGC	ATC	TTC	GAT	1584
6708	Il€	туг	Arg	, Phe	val val	. Thr	Pro	Gly	7 Glu	ı Arg	Pro	Sei	Gl3	, Met	t Phe	Asp	
6709			515	5				520)				525)			
6710					. .							י שמיי	ת ממי	n mar	2 ጥአር	י מאמ	1632
6711	TCC	TCC	GTC	CTC	rG7	GAC	TGC	TA'	GAC	. שטע הוא	, GGC	, La.	. GC1	י ביטי יו דיים	יעד מ ועד מ	GAG Glu	
6712	Sei	ser	· val	г гел	т сая	s GTI	ı cys	эт. Уг	. ADL	HIC	. от)	, суз]	1 -		

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6713		530					535					540					
6714																	
6715	CTC	ACC	CCC	GCC	GAG	ACC	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	1680
6716						Thr											
6717	545					550			3		555		- 2 -			560	
6718																	
6719	CCA	GGG	TTG	CCC	GTT	TGC	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	1728
6720						Cys											
6721	-				565					570					575		
6722																	
6723	TTC	ACA	GGC	CTC	ACC	CAT	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	1776
6724	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	
6725			_	580				_	585					590		-	
6726																	
6727	CAG	GCA	GGA	GAC	AAC	TTC	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	1824
6728	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	
6729			595					600					605				
6730																	
6731						GCC											1872
6732	Cys		Arg	Ala	Gln	Ala		Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	
6733		610					615					620					
6734																	
6735						AAA											1920
6736	-	Leu	тте	Arg	Leu	Lys	Pro	Thr	Leu	His	_	Pro	Thr	Pro	Leu		
6737 6738	625					630					635					640	
6739	መአሮ	NGG.	CTC	CCA	acc	GTC	מאא	חאא	GVG	GTC.	אממ	CTC	אממ	מאמ	aaa	א ייי א	1968
6740						Val											1900
6741	ı yı	nr 9	БСС	OLY	645	Val	OTIL	ASII	Giu	650	1111	пец	1111	1113	655	116	
6742					015					050					033		
6743	ACC	AAA	TAC	ATC	ATG	GCA	TGC	ATG	TCG	GCT	GAC	CTG	GAG	GTC	GTC	ACT	2016
6744						Ala											
6745			-	660			-		665					670			
6746																	
6747																	
6748																	
6749																	
6750																	
6751	(2)	TNEC	יאשמי	rton.	FOR	SEQ	TD 1	τO • 1 ·	2.						·		
6752	(2)	T.11E (- all'isti		1 010	250	10 1										
6753		(i)	SEC	OUEN	CE CE	IARAC	TER	STIC	cs:								
6754		, - ,	-			I: 64				5							
6755						nucl		_									
6756						DEDNE											
6757			•	•		OGY:			•								
6758			•														
6759		(ii)	MOI	LECUI	E TY	PE:	CDNA	A									
6760																	
6761																	
6762		(ix)		ATURE													
6763			•	•		KEY:											
6761			/ T) \ T /	10 x m 1		1 4										

(B) LOCATION: 1..648

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48
96
144
192
240
288

6793	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	336
6794	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	
6795				100					105					110			
6796																	
6797	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	384
6798	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	
6799			115					120		·			125				
6800																	
6801	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	432
6802	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	
6803		130					135					140					
6804																	
6805	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	480
6806	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	
6807	145					150					155					160	
6808																	
6809	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	528
6810	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	
6811					165					170					175		
6812																	
6813	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	576
6814	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	
6815				180					185				_	190			
6816																	
6817	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	624

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

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6818	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val		Val	Glu	Ser	
6819	-		195	-				200					205				
6820																	.
6821·	ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA									648
6822	Met	Glu	Thr	Thr	Met	Arg	Ser										
6823		210					215										
6824	•																
6825																	
6826																	
7236	(2)	INFO	ORMAT	TION	FOR	SEQ	ID 1	10:1	17:								
7237																	
7238		(i)) SEÇ														
7239									pair	s							
7240					PE:												
7241					rani				эте								
7242			(I	D) T(OPOLO	GY:	line	ear									
7243												i					
7244		(ii) MOI	LECU	LE T	PE:	CDN	4									
7245																	
7246																	
7247					_												
7248		(ix) FEA														
7249					AME/I												
7250			(I	B) Lo	OCAT:	con:	1	1941									
7251																	
7252												-					
7253		(Xi) SE	QUEN	CE DI	ESCR.	IPTI	ON:	SEQ .	LD NO): TT	/ :					
7254									~		ama	000	aaa	000	3.00	aaa	4.8
7255	ATG	CAT	ATG	CAT	CAT	CAT	CAC	CAT	CAT	CTG	GTG	Dea	3	Ø3	AGC Cor	λla	
7256		His	Met	His		His	HIS	HIS	HIS		var	PIO	Arg	СТУ	15	ATG	
7257	1				5					10					13		
7258							<i>a</i>	~~	200	999	aaa	CITE A	C TOTAL	aam	TOO	እጥሮ	96
7259	ccc	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	3	GGC	CIA	CII	Clu	Cvc	Tle	,
7260	Pro	ITe	Thr			ser	GIN	GIN		arg	σту	ьeu	ьeu	30		TTC	-
7261				20					25					30			
7262	~	. ~~		amm	3.02	000	000	030	224	224	CAC	CTC	GAC	GGA	GVG	GTT	144
7263	AAG	ACT	AGC	CTT	ACA	GGC	7-~	A ~~	AAG	AAC	CAG	Ual	יונט	GOA	Glu	Val	
7264	ьys	rnr	Ser		ınr	чΣУ	Arg		пλя	HSII	GTH	val	45	оту	JIU		
7265			35					40					. +3				
7266	a. c	ama	GTT	maa	3.00	00 ×	202	(1))	TOC	ጥጥረ	CTC	מממ	אממ	ጥርር	GTC	AAC	19:
7267	CAG	GTG	Val	TCC	ACC	GCA	ACA m⊾⊷	CAA	200	Dha	Lau	אוה	Thr	Cac	Va1	Asn	
7268	GIN			ser	Thr	ATG			ser	LIIG	ьeu	60	TIII	Cys	401	*2m11	
7269		50					55					60					
7270		~-~	m~-	m~~		ame	ma a	a s m	COM	O O E	aaa	TIC A	አአጣ	אממ	фπу	acc	24
7271	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	mh-	IIA	δla	2 4
7272	-		Cys	Trp	unr			nıs	стλ	ата		ser	ьys	1111	Ten	80	
7273	65	•				70					75					00	
7274						<u></u>		a	.	m = ~	3.00	3 3 m	ama	0.5.0	a s a	CAC	28
7275	GGC	CCA	. AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC	20
7276	Gly	Pro	Lys	GTA			rnr	GIN	мет			ASN	val	ASP		Asp	
7277					85					90					95		
7278																	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

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7279	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	336
7280	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	
7281				100					105					110			
7282																	
7283	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC	384
7284	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	
7285			115					120					125				
7286																	
7287					CGG												432
7288	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	
7289		130					135					140					
7290																	
7291					TAC												480
7292	_	Pro	Val	Ser	Tyr		Lys	GTÀ	Ser	Ser	_	GŢĀ	Pro	Leu	Leu	_	
7293	145					150					155					160	
7294	a a m			~.~			~~~										500
7295					GCT												528
7296	Pro	ser	сту	HIS	Ala	vaı	СТА	тте	Pne		АТа	АТа	val	cys		Arg	
7297 7298					165					170		•			175		
7299	aaa	CTT	ccc	220	GCG	CTC	CAC	th th th	CTC	CCC	СШХ	CAC	maa.	አመሮ	CAA	λCIT	576
7300					Ala												370
7301	GLY	val	ALG	180	AIG	Val	rop	riie	185	110	Val	GIU	Der	190	G1u	1111	
7302				100					103					170			
7303	АСТ	ATG	CGG	тст	CCG	GTC	ттс	ACG	GAC	AAC	TCA	TCC	ccc	CCG	GCC	GTA	624
7304					Pro												
7305			195					200	E				205				
7306																	
7307	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	672
7308					Gln												
7309		210					215					220		_		_	
7310																	
7311	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	720
7312	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
7313	225					230					235					240	
7314																	
7315					CCG												768
7316	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala		Leu	Gly	Phe	Gly		Tyr	
7317					245					250					255		
7318				~~.	~~~	~~=		~~~	~~~								016
7319					CAC												816
7320	мет	ser	ьys		His	GTĀ	тте	Asp		Asn	тте	Arg	unr		vaı	arg	
7321				260					265					270			
7322 7323	N.C.C	λmm	N CC	202	aaa	aaa	aca	ama	202	ш х С	m/cm	3 CC	mam	aaa	224	ատա	864
7323 7324					GGC Gly												004
732 4 7325	TIII	TTG	275	TIIL	сту	WIG	FIO	280	1111	TÀT	ser.	TITE	285	оту	гуз	FIIG	
7326			213					200					200				
7327	Сіпіп	GCC	СУТ	GGT	GGT	ጥርር	ጥርጥ	GGG	GGC	ССТ	ጥΔጥ	GAC	ΔͲሮ	מ יד מ	ΔͲΔ	ጥርነጥ	912
7328					Gly												712
7329		290		~ _	1	~ <u>1</u> U	295	1	1		- 1 -	300				-,5	
7330												200					
7331	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	960

7378

7381 7382

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7332		Glu	Cys	His	Ser		Asp	Ser	Thr	Thr		Leu	Gly	Ile	Gly		
7333	305					310					315					320	
7334	ama	ama	a.a	a. .	000	a.a		aam					ama	~~~	ama	aaa	1000
7335									GGA								1008
7336	vaı	Leu	Asp	GIN		GIU	Thr	Ата	Gly		Arg	Leu	vaı	val		АТа	
7337					325					330					335		
7338	3.00	aam	3.00	aam	000	aa 8	maa	ama	3.00	ama	aa.	a.a	003		3.00	ara	1056
7339									ACC								1056
7340	Thr	ATG	THE		Pro	сту	ser	vaı	Thr	vaı	Pro	HIS	Pro		тте	GIU	
7341 7342				340					345					350			
7342	CAC.	CITIC	aaa	·CITIC	mom.	3 A TT	y GW	CCA	GAG	N III CI	000	mma	m's m	aaa	* * *	000	1104
7343									Glu								1104
7344	GIU	vaı	355	Leu	per	ASII	1111	360	GIU	116	PIO	File	365	СТА	гуѕ	ATA	
7345			333					300					303				
7347	איזירי	כככ	λητη	GAA	acc	איזיכי	A C C	aaa	GGA	MGG	CAT	CTC	አጥጥ	ጥጥረ	ጥርጥ	СУТ	1152
7348									Gly								1152
7349	116	370	116	010	ALG	116	375	оту	GLY	Arg	1113	380	116	1 116	Cys	1115	
7350	*	0,0					3,3					500					
7351	TCC	AAG	AAG	AAG	TGC	GAC	GAG	СТС	GCC	GCA	AAG	СТС	TCA	GGC	СТС	GGA	1200
7352									Ala								2200
7353	385	-1-	-1-	-1-	-7-	390					395			- -,		400	
7354																	
7355	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	1248
7356									Gly								
7357					405	•	•		•	410	•				415		
7358																	•
7359	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC	1296
7360	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	
7361				420					425					430			
7362												•					
7363	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC	1344
7364	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	
7365			435					440					445				
7366																	
7367									CCC								1392
7368	Gln		Val	Asp	Phe	Ser		Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	
7369		450					455					460					
7370																	
7371	_	_		_					CGC								1440
7372		Val	Pro	Gln	Asp		Val	Ser	Arg	Ser		Arg	Arg	Gly	Arg		
7373	465					470					475					480	
7374																	
7375									AGG								1488
7376	GТĀ	Arg	GTÀ	Arg	_	GTÀ	Ile	Tyr	Arg		Val	Thr	Pro	GLy		Arg	
7377					485					490					495		

7379 CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG

7380 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala

7383 GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG

7384 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999 TIME: 14:06:55

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7386																	
7387	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	CAG	GAC	CAC	CTG	1632
7388	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	
7389	_	530	_				535	_				540		_			
7390																	
7391	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	ATA	GAT	GCA	CAC	1680
7392	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His	
7393	545		_			550			_		555			-		560	
7394																	
7395	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	CCC	TAC	CTG	GTA	1728
7396	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val	
7397					565	-			_	570				•	575		
7398																	
7399	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	CCA	CCT	CCA	TCA	1776
7400	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arq	Ala	Gln	Ala	Pro	Pro	Pro	Ser	
7401		-		580			•		585					590			
7402																	
7403	TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	CCT	ACG	CTG	CAC	1824
7404	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His	
7405	-	-	595		-	-	-	600		•		•	605				
7406																	
7407	GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC	CAA	AAT	GAG	GTC	1872
7408	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val	
7409	_	610					615			-		620					
7410																	
7411	ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA	TGC	ATG	TCG	GCC	1920
7412	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala	
7413	625					630		-	-		635		-			640	
7414																	
7415	GAC	CTG	GAG	GTC	GTT	ACG	TAG										1941
7416	Asp	Leu	Glu	Val	Val	Thr											
7417	_				645												
7418																	
7419																	
7420																	
7974	(2)	INF	ORMA'	rion	FOR	SEQ	ID I	NO:12	21:								· · · · · · · · · · · · · · · · · · ·
7975																	•
7976		(1	•	QUEN	_												
7977				A) LI													
7978				3) T													
7979				C) S					gre								
7980			(1	D) T(OPOL	OGY:	line	ear									
7981																	
7982		(11)) MOI	LECUI	LE TY	PE:	RNA	(gei	nomi	2)							
7983																	
7984																	
7985																	
7986																	
												-					
7987 7988		(Xi) SE(QUEN	CE DE	ESCR	IPTI	on: :	SEQ :	ID NO	0:12	l:					

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GCUCGCCCGG GGAUCCUCUA GGAAUACACG UUCGAU

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